AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method of identifying genetic mutations that are associated with ataxic neurological disease in a ~~mammalian~~ human subject, said method comprising:

(a) determining a first nucleic acid sequence of a human protein kinase C gamma gene from a first human subject exhibiting ataxia;

(b) identifying a difference between [[a]] the first nucleic acid sequence ~~of a protein kinase C gamma gene~~ from [[a]] the first ~~mammalian~~ human subject exhibiting ataxia and SEQ ID NO:3 ~~a second nucleic acid sequence of a protein kinase C gamma gene from a second mammalian subject which is not exhibiting ataxia, wherein the first and second mammalian subjects are members of the same species, and wherein the difference between the nucleic acid sequences represents a genetic mutation in the first nucleic acid sequence that is associated with ataxic neurological disease~~; and

(c) confirming that the difference identified between the first nucleic acid sequence and SEQ ID NO:3 is a genetic mutation associated with ataxia by co-segregation analysis comprising determining that the identified nucleic acid sequence difference is also present in a plurality of human subjects exhibiting ataxia and is absent in a plurality of human subjects not exhibiting ataxia.

2. (Currently amended) The method of Claim 1 wherein the first nucleic acid sequence [[of]] from said first human subject ~~and said second subject~~ is determined by amplification of portions of the human protein kinase C gamma [[genes]] gene from genomic DNA isolated from said ~~subjects~~ human subject to produce an amplified DNA and sequencing said amplified DNA.

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3. (Canceled)

4. (Currently amended) The method of [[Claim 3]] Claim 1 wherein said cosegregation ~~is detected by~~ analysis comprises a method selected from the group consisting of direct sequencing, sequencing PCR-amplified DNA, single stranded conformation analysis, allele-specific PCR and restriction fragment length polymorphism.

5. (Currently amended) The method of Claim 4 wherein said cosegregation ~~is detected by~~ analysis comprises sequencing PCR-amplified DNA.

6. (Currently amended) The method of Claim 4 wherein said cosegregation ~~is detected by~~ analysis comprises restriction fragment length polymorphism ~~wherein the presence of an aberrant restriction enzyme site is indicative of the presence of said genetic mutation and cosegregation is determined by the presence of said genetic mutation in a first population of mammalian subjects that exhibit ataxia and not present in a second population of subjects that do not exhibit ataxia~~.

7-42. (Canceled)

43. (New) The method of Claim 2, wherein the portions of nucleic acid sequence that are amplified comprises at least one of exon 1 (nucleotides 440 to 609 of SEQ ID NO:3); exon 2 (nucleotides 1108 to 1139 of SEQ ID NO:3); exon 3 (nucleotides 2106 to 2188 of SEQ ID NO:3); exon 4 (nucleotides 7583 to 7694 of SEQ ID NO:3) ; exon 5 (nucleotides 7831 to 7962 of SEQ ID NO:3); exon 6 (nucleotides 9619 to 9775 of SEQ ID NO:3); exon 7 (nucleotides 10454 to 10588 of SEQ ID NO:3); exon 8 (nucleotides 10933 to 11020 of SEQ ID NO:3); exon 9 (nucleotides 11307 to 11336 of SEQ ID NO:3); exon 10 (nucleotides 15904 to 16056 of SEQ ID NO:3); exon 11 (nucleotides 16385 to 16573 of SEQ ID NO:3); exon 12 (nucleotides 18178 to 18269 of SEQ ID NO:3); exon 13 (nucleotides 18364 to 18426 of

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SEQ ID NO:3); exon 14 (nucleotides 18556 to 18694 of SEQ ID NO:3); exon 15 (nucleotides 21018 to 21098 of SEQ ID NO:3); exon 16 (nucleotides 22580 to 22687 of SEQ ID NO:3); exon 17 (nucleotides 24262 to 24402 of SEQ ID NO:3); or exon 18 (nucleotides 24652 to 24840 of SEQ ID NO:3).

44. (New) The method of Claim 43, wherein the portion of SEQ ID NO:3 that is amplified comprises exon 4 (nucleotides 7583 to 7694 of SEQ ID NO:3).

45. (New) The method of Claim 1, wherein the mutation associated with ataxia neurological disease is selected from the group consisting of a missense mutation, a deletion mutation, an insertion mutation, a splicing site mutation, and a mutation that results in loss of expression of the protein kinase C gamma gene encoded by SEQ ID NO:3.

46. (New) The method of Claim 45, wherein the mutation is a missense mutation.

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